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Cardiac Electrophysiology Numerical Models using symmetric multiprocessing (SMP)

Stefanos Konstantinos D. Petsios, *Student Member, IEEE* and Dimitrios I. Fotiadis, *Senior Member, IEEE*

***Abstract*— Multi-dimensional electrophysiological models have been introduced to investigate electrical propagation in tissue level, based on cell-dynamics models. The models include a set of non-linear differential equations which describe the dynamics of cell and tissue excitation. However, as models evolve, it is inevitable that proper and powerful tools need to be introduced in order to reproduce the detailed and thus computationally intensive simulations. To build such tools, several computational methodologies need to be adopted regarding efficiency and reliability. On the other hand improvements apply to the hardware too. State of the art computers, even personal computers, tend to make use of multiple core Central Processing Units. Unfortunately the aforementioned methodologies follow sequential logic, resulting to low efficiency of the working platform. In this work we present the performance bottleneck in symmetric multiprocessing (SMP) for simulations of propagation phenomena in cardiac tissue electrophysiological models. We demonstrate the scalability and efficacy of the different methodologies used in the discretisation scheme and message passing in SMP.**

I. Introduction

ADVANCES in cellular electrophysiology have resulted in an increased demand for computationally efficient simulations for the evaluation of advanced multidimensional electrophysiological models. In the last decades a vast amount of complex physiological functions and corresponding models have been developed in cell, tissue and organ level. Computational demands, under specific circumstances may be overwhelmed by distributed computations. An approximate unit to quantify the computational load of a full heart beat is the number of required floating point operations. For example to simulate the electrical activity of a heart beat lasting about one second with time step 0.01msec and space slice 0.1mm would require approximately 10^{16} floating point operations. Experiments that require several heart beats will linearly increase this requirement. Simulating a full pacing protocol consisting of 17 beats over 3 seconds tissue space 14 x 14 mm^2 and consisting of 78961 discrete points, typically requires 10 - 15 hours of computation using the CMISS (Continuum Mechanics, Image analysis, Signal processing and System Identification) with as many as 32 possessors on a high performance computer (IBM Regatta with 50 P5, 1.9 GHz processors and 210 GB shared memory) [1]. Fine spatial detail or more complex dynamics will exponentially increase the computational load. The current trend in electrophysiological modeling is to express and exchange biological models using extended mark up languages like CellML [2] and SBML [3]. We have studied a variety of tools performing cell tissue simulations: OxSoft Heart [4], E-Cell [5] [6] SimTool, Gepasi, STOCKS, StochSim, MCell [7], PROTOPLASM [8]. All these tools cover different needs and no direct comparison can be performed. Frameworks enabling the handling of such models have been presented in the literature, however they focus in 0D [9] or 1D experiments and limited functionality is available in order to carry out 2D or 3D experiments [10]. Besides that, most of the available frameworks do not support multiprocessing computations. This work is based on a software framework named BioPSiS [11] which enables evaluation of the proposed methods. We used this framework to quantify the load and differences between the parameters causing the extra computational bottleneck during the numerical integration with the help of symmetric multiprocessing (SMP). More specifically, we study the relevance of the propagation phenomena in cardiac tissue and the discretisation scheme with the computational bottleneck of SMP in terms of processing efficiency. In this work we present the role of propagation phenomena in two dimensional cardiac tissue.

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S.D. Petsios is with Department of Computer Science, University of Ioannina, GR 45110 Ioannina, Greece stefanos@cs.uoi.gr, fotiadis@cs.uoi.gr

D. I. Fotiadis is with the Unit of Medical Technology and Intelligent Information Systems, Department of Materials Science and Engineering, University of Ioannina, GR 45110 Ioannina, Greece fotiadis@cs.uoi.gr

II. Background

A. Description of the electrophysiological problem

The mechanical activity of the heart is triggered by waves of excitation initiated at the sinoatrial node spreading through the atrial tissue, the atrioventicular node and the ventricular wall. The excitation waves are generated by membrane currents and spread by local circuit currents through the intracellular and extracellular space. The models of propagation in cardiac tissue must consider local excitation and excitation spread mechanisms. Thus, proper coupled ordinary differential equations models are based on detailed biophysical excitation models and have been used to describe both local properties and global spatiotemporal properties of the cardiac tissue.

Discrete models of propagation in cardiac tissue involve cellular automata. A cellular automaton represents the state of a cell with a discrete set of values over a discrete time domain. The evolution of the cell state follows a deterministic rule which relates its state S_{n+1} at the discrete time step *n+1* with its state S_n and the states of its neighbors at the

previous time step n. In Fig. 1 we depict this evolution in 1D tissue models. In order to reproduce electrophysiological waveforms, mechanisms and velocity curvature effects, the discrete models use ordinary differential equation (ODE) models. Such models can provide an accurate description of both local temporal properties and global spatiotemporal properties of cardiac tissue but they are extremely demanding in terms of computational power.

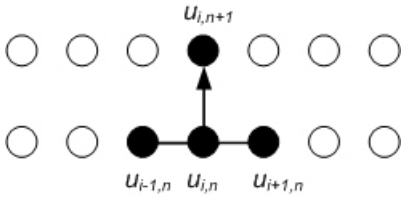

Fig. 1. Discretisation scheme for one-dimensional excitable media.

B. Symmetric Multiprocessing Computations

To achieve higher performance for complex simulations, parallelization is required. The most popular method is to provide several identical execution units that can all process a task. Concerning the operating system, SMP is able to set up any task on any of the processors available. SMP systems have no master or slave processors and each logical unit is able to complete a given task. It is up to the programmer to make sure that the processors are used to their maximum potential. A common conception is that SMP programming is much simpler as any processor in the system can complete a given task, thus a programmer just needs to balance the estimated workload between processors.

Operating systems that implement symmetric multiprocessing (SMP) are capable to distribute dynamically the tasks to the available processors. In this paper we present the results of two proposed methodologies for task distribution and their efficiency against various propagation conditions.

III. Design and implementation of the Computational Framework

A. Discretisation schemes

An important step is the discretisation scheme for the model. Discretisation of both space and time is needed. If we discretise space and time using sufficiently small steps Δx, Δt, then in one dimensional excitable medium at each point in space at the following time step the value of its present value, as well as, the values of its two closest neighbors in space at the present time are needed.

In two dimensional excitable media the wave patterns and behavior are much enriched as propagation velocity depends on curvature. The discretisation schemes for two dimensional propagation can be defined with 5 or 9 grid point values in order to calculate the diffusion term. In Figs. 2 and 3 the two patterns are shown.

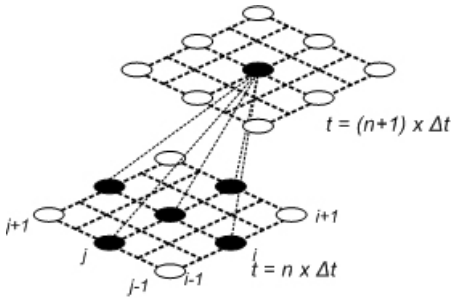

Fig. 2. 5-point discretisation scheme.

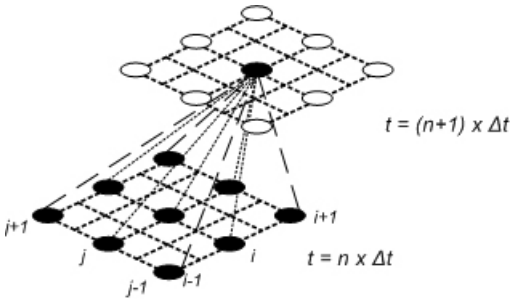

Fig. 3. 9-point discretisation scheme.

B. The measurement and processing subsystem

The BioPSiS framework is used to implement the proposed methodology. In Fig. 4 we present the added component named *measurement and benchmarking processor* to the *Computation Processor* subsystem of BioPSiS in order to support precise and thorough measurements. The measurement and processing system is implemented as a special subsystem of BioPSiS, capable to provide us with reliable measurements and flexibility to accomplish the experiments. The implemented components were custom made in order to compare the computational bottleneck between the proposed methodologies and two different two dimensional propagation models. Due to this measurement component a notable overhead applies to the solver but real time corrections are made.

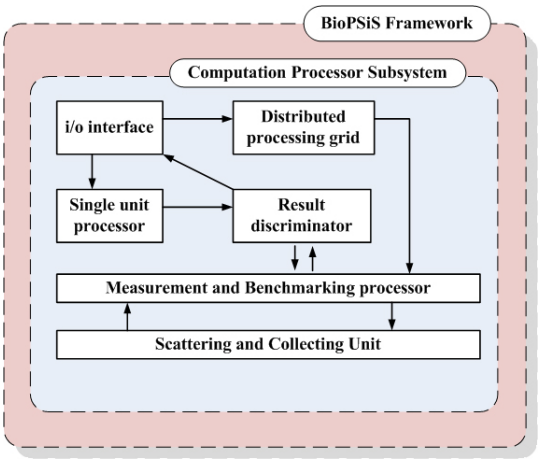

Fig. 4. Computation processor subsystem architecture.

IV. Implemented methods

A computational physiological model of excitation kinetics is generally formulated as a set of ordinary differential equations in the Cell level and a set of partial differential equations in the tissue level. In addition, a set of initial conditions is needed. The steps of the sequential simulation protocol (non-SMP) are:

- The cell level equations expressed in mathml files are converted to program code.
- The structure of the tissue is defined.
- The Propagation phenomena of cardiac tissue are expressed with algebraic equations and converted to program code.
- The calculation procedure of the solver is defined.

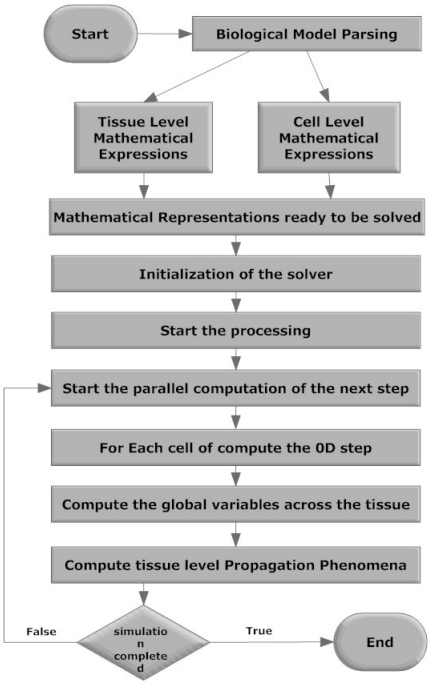

Fig. 5. Flowchart for the sequential numerical processing.

In order to implement symmetrical multiprocessing functionality to the aforementioned steps, proper parallelizing techniques are applied. Each one of the aforementioned steps needs to be extended, these extensions are not straightforward and different decisions could be made in critical steps of the process and separate strategies - algorithms - methodologies that can be followed according to: meshing, scheduling, synchronization, message passing and race conditions.

For example the meshing schemes are strongly correlated to the efficiency of SMP calculations and will directly affect the parallelization efficiency. In the present work we focus our study on the role of the propagation phenomena in the SMP simulations and no complicated or special meshing was used.

With the help of flowchart diagrams in Fig. 5 and Fig. 6, we depict the algorithmic steps of two implementations

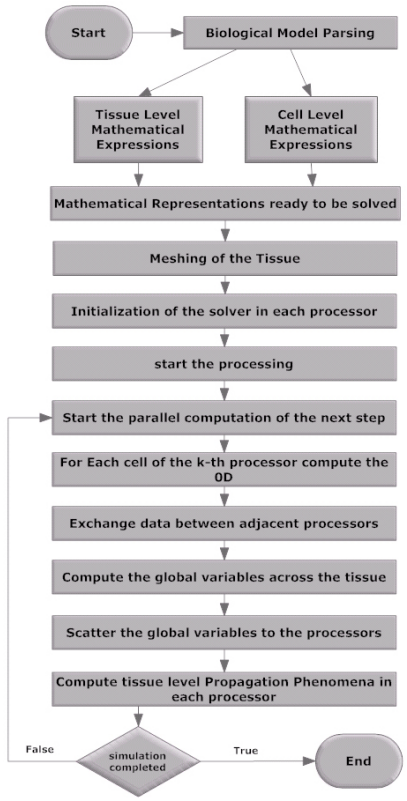

Fig. 6. Flowchart for the parallel numerical processing

based on single and parallel processing, notable differences between the two algorithms are focused in the propagation phenomena. In the parallel processing, after the initial meshing of our tissue we scatter and gather information once in each simulation step, since the calculation of global variables for the propagation phenomena step is needed. Scattering of the results is performed and the propagation step is applied on each node. Finally message passing between adjacent nodes is needed, in order to exchange local excitation results.

V. Experiments

The scope of this work is to create algorithms that can speed up the simulation process. In this work we used as a case study a two dimensional grid of 50 nodes width and 50 nodes length, representing cardiac muscle excitation. The duration of the simulation was 300 time steps (3 sec with 0.01sec time step). In each step a parabolic reaction-diffusion equation is solved where the voltage across the cell membrane is calculated.

Simulation experiments were performed using BioPSiS by implementing a custom made multiprocessing simulator for each case. The experiments were made in two different environments. First using a solver based on posix threads installed on a personal computer with Quad Core technology. Second using a small grid of 8 identical workstations is used and a solver based in Message Passing Interface (MPI) on a Beowulf like cluster is employed.

In Table I we present the results measured in minutes for each experiment. For each experiment we measured the

TABLE I

BENCHMARK TABLE BETWEEN THE VARIOUS ARCHITECTURES FOR TWO DISCRETISATION SCHEMES

Architecture	5-point scheme		9-point scheme	
1CPU	18	410	34	432
2CPU SMP 2 threads	22	227	37	253
4CPU SMP 4 threads	28	130	55	163
4CPU SMP 16 threads	36	138	72	180
1 Node in Beowulf Cluster	23	522	43	551
8 Nodes in Beowulf Cluster	49	101	91	160

computation time needed for the application of propagation phenomena steps and the total time of each experiment.

VI. DISCUSSION

Converting the sequential numerical processing in SMP derives two primary computation restrictions. First the parallelization demands extra message passing between the processes which is highly dependent on the selected meshing scheme. For example in 1D meshing, message passing usually involves only two neighbors. Adding an extra dimension in the simulation, the meshing and discretisation schemes increase the complexity and the different strategies which must be used. The multiprocessing environment with the help of proper algorithms reduces the total computational time to apply propagation phenomena in each step. These algorithms are highly correlated with the meshing and the equations of the propagation phenomena, thus no such algorithm was implemented.

Table 1 shows that adding processors to the solver speed up the simulation in both discretisation schemes. In the case of 4 CPUs with 4 threads, the speedup for the 5-point scheme is 3.15 times faster than the single processing unit. The propagation time was 18 minutes for the single processing and 28 minutes for the 4 CPU SMP, meaning 10 minutes overhead in 130 minutes of complete execution time (7.6%). In the 9 point scheme we achieved 2.65 times speedup. The propagation time was 34 minutes for the single processing and 55 minutes in the 4 CPU SMP, meaning 19 minutes overhead in 163 minutes of complete execution time (11.6%).

The increase of points used for the discretisation scheme resulted in an increase of floating point operations to be solved. In the single processing environments an approximately 5% increase in total execution time was found. Comparing the 4 CPU SMP environments the respective increase was 20%. The processing time to apply the propagation phenomena is longer than the time of the the single processing architecture. This happens because of the message passing between the nodes.

VII. CONCLUSIONS

With the advances in hardware resources based on SMP, even at personal computer level, the need for methods capable to exploit the resources in electrophysiological cell and tissue modeling has emerged. The current solvers are based on sequential execution of imperative languages. The computational parallelization from cell level (0D) to tissue level (1D, 2D, 3D) simulations should be implemented to the modern frameworks. To achieve this in a computational level, a proper imperative work flow must be followed. Typically the end users of such frameworks are not trained to produce parallelization schemes or algorithms. Thus semi automated or fully automated methods must be integrated into the frameworks. The efficiency of those algorithms is important, so further studies need to quantify the role of other computational parameters that apply in the numerical computational process. Moreover, the existing specifications which describe cell and tissue level biological models must be enriched with formalized declarative or procedural expressions that will act as a guideline to produce semi-automated efficient computational frameworks.

VIII. ACKNOWLEDGMENTS

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